

**Amendments to the Specification:**

Please amend the paragraph beginning on page 6, line 21 as follows:

Figure 1E shows the results of assays of the ability of serial substitution mutants of GST-CH1 (amino acids 302-528) produced as GST fusion proteins, with the sequence NAAIRS (SEQ ID NO: 1) inserted in place of the indicated amino acids, to bind to IVT full length HIF-1 $\alpha$ .

Please amend the paragraph beginning on page 18, line 16 as follows:

To study further the requirements for HIF-1 $\alpha$ /CH I binding, a series of GST-CH1 (amino acids 302-528) internal substitution mutants were generated. These serial, non-overlapping mutants spanned residues 341-424 of p300. In each mutant, five residues were deleted and the sequence, Asp-Ala-Ala-Ile-Arg-Ser (NAAIRS, SEQ ID NO: 1), inserted. The NAAIRS sequence can assume an  $\alpha$ -helical or  $\beta$ -strand conformation (Wilson et al., Proc. Natl. Acad. Sci. U.S.A. 82:5255-5259, 1985), thus, decreasing the likelihood of generalized conformational disruption following the deletion/insertion event. Almost all substitutions abolished CH I binding to full length HIF-1 $\alpha$  (Figure 1E), suggesting that the CH1 domain must assume a complex, zinc-coordinated conformation in order to interact with HIF-1 $\alpha$ .

Please insert the sequence listing at the end of the specification.